



## SEQUENCE LISTING

RECEIVED

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TECH CENTER 1600/2900

<110> Willson, Tracy  
Nicola, Nicos A.  
Hilton, Douglas J.  
Metcalf, Donald  
Zhang, Jian G.

<120> NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES  
ENCODING SAME

<130> Davies Collison Cave

<140> 09/688,286  
<141> 2000-10-13

<150> 09/051,843  
<151> 1998-06-29

<160> 11

<170> PatentIn Ver. 2.0

<210> 1  
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<212> DNA  
<213> Unknown Organism

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of mNR4

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<222> (61)..(1338)

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<222> (121)  
<223> n-authors are unsure of exact sequence in this  
region

<220>  
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atg gcg cg<sup>g</sup> cca gc<sup>g</sup> ctg ctg ggc gag ctg ttg gtg ctg cta ctg tgg 108  
Met Ala Arg Pro Ala Leu Leu Gly Glu Leu Leu Val Leu Leu Leu Trp  
1 5 10 15

acc gcc acc gtg nn<sup>n</sup> ggc caa gtt gcc gc<sup>g</sup> gcc aca gaa gtt cag cca 156  
Thr Ala Thr Val Xaa Gly Gln Val Ala Ala Ala Thr Glu Val Gln Pro  
20 25 30

cct gtg acg aat ttg agc gtc tct gtc gaa aat ctc tgc acg ata ata 204  
Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Ile Ile  
35 40 45

tgg acg tgg agt cct cct gaa gga gcc agt cca aat tgc act ctc aga 252  
Trp Thr Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg  
50 55 60

tat ttt agt cac ttt gat gac caa cag gat aag aaa att gct cca gaa 300  
Tyr Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu  
65 70 75 80

act cat cgt aaa gag gaa tta ccc ctg gat gag aaa atc tgt ctg cag		348
Thr His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln		
85	90	95
gtg ggc tct cag tgt agt gcc aat gaa agt gag aag cct agc cct ttg		396
Val Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu		
100	105	110
gtg aaa aag tgc atc tca ccc cct gaa ggt gat cct gag tcc gct gtg		444
Val Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val		
115	120	125
act gag ctc aag tgc att tgg cat aac ctg agc tat atg aag tgt tcc		492
Thr Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser		
130	135	140
tgg ctc cct gga agg aat aca agc cct gac aca cac tat act ctg tac		540
Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr His Tyr Thr Leu Tyr		
145	150	155
160		
tat tgg tac agc agc ctg gag aaa agt cgt caa tgt gaa aac atc tat		588
Tyr Trp Tyr Ser Ser Leu Glu Lys Ser Arg Gln Cys Glu Asn Ile Tyr		
165	170	175
aga gaa ggt caa cac att gct tgt tcc ttt aaa ttg act aaa gtg gaa		636
Arg Glu Gly Gln His Ile Ala Cys Ser Phe Lys Leu Thr Lys Val Glu		
180	185	190
cct nnn agt ttt gaa cat cag aac gtt caa ata atg gtc aag gat aat		684
Pro Xaa Ser Phe Glu His Gln Asn Val Gln Ile Met Val Lys Asp Asn		
195	200	205
gct ggg aaa att agg cca tcc tgc aaa ata gtg tct tta act tcc tat		732
Ala Gly Lys Ile Arg Pro Ser Cys Lys Ile Val Ser Leu Thr Ser Tyr		
210	215	220
gtg aaa cct gat cct cca cat att aaa cat ctt ctc ctc aaa aat ggt		780
Val Lys Pro Asp Pro His Ile Lys His Leu Leu Leu Lys Asn Gly		
225	230	235
240		
gcc tta tta gtg cag tgg aag aat cca caa aat ttt aga agc aga tgc		828
Ala Leu Leu Val Gln Trp Lys Asn Pro Gln Asn Phe Arg Ser Arg Cys		
245	250	255
tta act tat gaa gtg gag gtc aat aat act caa acc gac cga cat aat		876
Leu Thr Tyr Glu Val Glu Val Asn Asn Thr Gln Thr Asp Arg His Asn		
260	265	270

att tta gag gtt gaa gag gac aaa tgc cag aat tcc gaa tct gat aga		924
Ile Leu Glu Val Glu Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arg		
275	280	285
aac atg gag ggt aca agt tgt ttc caa ctc cct ggt gtt ctt gcc gac		972
Asn Met Glu Gly Thr Ser Cys Phe Gln Leu Pro Gly Val Leu Ala Asp		
290	295	300
gct gtc tac aca gtc aga gta aga gtc aaa aca aac aag tta tgc ttt		1020
Ala Val Tyr Thr Val Arg Val Arg Val Lys Thr Asn Lys Leu Cys Phe		
305	310	315
320		
gat gac aac aaa ctg tgg agt gat tgg agt gaa gca cag agt ata ggt		1068
Asp Asp Asn Lys Leu Trp Ser Asp Trp Ser Glu Ala Gln Ser Ile Gly		
325	330	335
aag gag caa aac tcc acc ttc tac acc acc atg tta ctc acc att cca		1116
Lys Glu Gln Asn Ser Thr Phe Tyr Thr Thr Met Leu Leu Thr Ile Pro		
340	345	350
gtc ttt gtc gca gtg gca gtc ata atc ctc ctt ttt tac ctg aaa agg		1164
Val Phe Val Ala Val Ala Val Ile Ile Leu Leu Phe Tyr Leu Lys Arg		
355	360	365
ctt aag atc att ata ttt cct cca att cct gat cct ggc aag att ttt		1212
Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe		
370	375	380
aaa gaa atg ttt gga gac cag aat gat gat acc ctg cac tgg aag aag		1260
Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys		
385	390	395
400		
tat gac atc tat gag aaa caa tcc aaa gaa gaa acg gat tct gta gtg		1308
Tyr Asp Ile Tyr Glu Lys Gln Ser Lys Glu Glu Thr Asp Ser Val Val		
405	410	415
ctg ata gaa aac ctg aag aaa gca gct cct tgatggggag aagtgattc		1358
Leu Ile Glu Asn Leu Lys Lys Ala Ala Pro		
420	425	
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<212> DPT

<213> Unknown Organism

<220>

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of mNR4

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<221> unsure

<222> (21)

<223> authors are unsure about the sequence assignment

<220>

<221> unsure

<222> (194)

<223> authors are unsure about the sequence assignment

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1 5 10 15

Thr Ala Thr Val Xaa Gly Gln Val Ala Ala Ala Thr Glu Val Gln Pro  
20 25 30

Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Ile Ile  
35 40 45

Trp Thr Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg  
50 55 60

Tyr Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu  
65 70 75 80

Thr His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln  
85 90 95

Val Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu  
100 105 110

Val Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val  
115 120 125

Thr Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser  
130 135 140

Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr His Tyr Thr Leu Tyr  
145 150 155 160

Tyr Trp Tyr Ser Ser Leu Glu Lys Ser Arg Gln Cys Glu Asn Ile Tyr  
165 170 175

Arg Glu Gly Gln His Ile Ala Cys Ser Phe Lys Leu Thr Lys Val Glu  
180 185 190

Pro Xaa Ser Phe Glu His Gln Asn Val Gln Ile Met Val Lys Asp Asn  
195 200 205

Ala Gly Lys Ile Arg Pro Ser Cys Lys Ile Val Ser Leu Thr Ser Tyr  
210 215 220

Val Lys Pro Asp Pro Pro His Ile Lys His Leu Leu Leu Lys Asn Gly  
225 230 235 240

Ala Leu Leu Val Gln Trp Lys Asn Pro Gln Asn Phe Arg Ser Arg Cys  
245 250 255

Leu Thr Tyr Glu Val Glu Val Asn Asn Thr Gln Thr Asp Arg His Asn  
260 265 270

Ile Leu Glu Val Glu Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arg  
275 280 285

Asn Met Glu Gly Thr Ser Cys Phe Gln Leu Pro Gly Val Leu Ala Asp  
290 295 300

Ala Val Tyr Thr Val Arg Val Arg Val Lys Thr Asn Lys Leu Cys Phe  
305 310 315 320

Asp Asp Asn Lys Leu Trp Ser Asp Trp Ser Glu Ala Gln Ser Ile Gly  
325 330 335

Lys Glu Gln Asn Ser Thr Phe Tyr Thr Thr Met Leu Leu Thr Ile Pro  
340 345 350

Val Phe Val Ala Val Ala Val Ile Ile Leu Leu Phe Tyr Leu Lys Arg  
355 360 365

Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe  
370 375 380

Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys  
385 390 395 400

Tyr Asp Ile Tyr Glu Lys Gln Ser Lys Glu Glu Thr Asp Ser Val Val  
405 410 415

Leu Ile Glu Asn Leu Lys Lys Ala Ala Pro  
420 425

<210> 3  
<211> 1383  
<212> DNA  
<213> Unknown Organism

<220>  
<223> Description of Unknown Organism:Human IL-13 receptor  
alpha-chain

<220>  
<221> CDS  
<222> (61)..(1338)

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Met Glu Trp Pro Ala Arg Leu Cys Gly Leu Trp Ala Leu Leu Leu Cys  
1 5 10 15  
gcc ggc ggc ggg ggc ggg ggc ggc gcg cct acg gaa act cag cca 156  
Ala Gly Gly Gly Gly Gly Gly Ala Pro Thr Glu Thr Gln Pro  
20 25 30  
cct gtg aca aat ttg agt gtc tct gtt gaa aac ctc tgc aca gta ata 204  
Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile  
35 40 45  
tgg aca tgg aat cca ccc gag gga gcc agc tca aat tgt agt cta tgg 252  
Trp Thr Trp Asn Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu Trp  
50 55 60  
tat ttt agt cat ttt ggc gac aaa caa gat aag aaa ata gct ccg gaa 300  
Tyr Phe Ser His Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro Glu  
65 70 75 80  
act cgt cgt tca ata gaa gta ccc ctg aat gag agg att tgt ctg caa 348  
Thr Arg Arg Ser Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln  
85 90 95  
gtg ggg tcc cag tgt agc acc aat gag agt gag aag cct agc att ttg 396  
Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu  
100 105 110

gtt gaa aaa tgc atc tca ccc cca gaa ggt gat cct gag tct gct gtg		444
Val Glu Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val		
115	120	125
act gag ctt caa tgc att tgg cac aac ctg agc tac atg aag tgt tct		492
Thr Glu Leu Gln Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser		
130	135	140
tgg ctc cct gga agg aat acc agt ccc gac act aac tat act ctc tac		540
Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr		
145	150	155
160		
tat tgg cac aga agc ctg gaa aaa att cat caa tgt gaa aac atc ttt		588
Tyr Trp His Arg Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile Phe		
165	170	175
aga gaa ggc caa tac ttt ggt tgt tcc ttt gat ctg acc aaa gtg aag		636
Arg Glu Gly Gln Tyr Phe Gly Cys Ser Phe Asp Leu Thr Lys Val Lys		
180	185	190
gat tcc agt ttt gaa caa cac agt gtc caa ata atg gtc aag gat aat		684
Asp Ser Ser Phe Glu Gln His Ser Val Gln Ile Met Val Lys Asp Asn		
195	200	205
gca gga aaa att aaa cca tcc ttc aat ata gtg cct tta act tcc cgt		732
Ala Gly Lys Ile Lys Pro Ser Phe Asn Ile Val Pro Leu Thr Ser Arg		
210	215	220
gtg aaa cct gat cct cca cat att aaa aac ctc tcc ttc cac aat gat		780
Val Lys Pro Asp Pro Pro His Ile Lys Asn Leu Ser Phe His Asn Asp		
225	230	235
240		
gac cta tat gtg caa tgg gag aat cca cag aat ttt att agc aga tgc		828
Asp Leu Tyr Val Gln Trp Glu Asn Pro Gln Asn Phe Ile Ser Arg Cys		
245	250	255
cta ttt tat gaa gta gaa gtc aat aac agc caa act gag aca cat aat		876
Leu Phe Tyr Glu Val Glu Val Asn Asn Ser Gln Thr Glu Thr His Asn		
260	265	270
gtt ttc tac gtc caa gag gct aaa tgt gag aat cca gaa ttt gag aga		924
Val Phe Tyr Val Gln Glu Ala Lys Cys Glu Asn Pro Glu Phe Glu Arg		
275	280	285
aat gtg gag aat aca tct tgt ttc atg gtc cct ggt gtt ctt cct gat		972
Asn Val Glu Asn Thr Ser Cys Phe Met Val Pro Gly Val Leu Pro Asp		
290	295	300

act ttg aac aca gtc aga ata aga gtc aaa aca aat aag tta tgc tat		1020	
Thr Leu Asn Thr Val Arg Ile Arg Val Lys Thr Asn Lys Leu Cys Tyr			
305	310	315	320
gag gat gac aaa ctc tgg agt aat tgg agc caa gaa atg agt ata ggt		1068	
Glu Asp Asp Lys Leu Trp Ser Asn Trp Ser Gln Glu Met Ser Ile Gly			
325	330	335	
aag aag cgc aat tcc aca ctc tac ata acc atg tta ctc att gtt cca		1116	
Lys Lys Arg Asn Ser Thr Leu Tyr Ile Thr Met Leu Leu Ile Val Pro			
340	345	350	
gtc atc gtc gca ggt gca atc ata gta ctc ctg ctt tac cta aaa agg		1164	
Val Ile Val Ala Gly Ala Ile Ile Val Leu Leu Leu Tyr Leu Lys Arg			
355	360	365	
ctc aag att att ata ttc cct cca att cct gat cct ggc aag att ttt		1212	
Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe			
370	375	380	
aaa gaa atg ttt gga gac cag aat gat gat act ctg cac tgg aag aag		1260	
Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys			
385	390	395	400
tac gac atc tat gag aag caa acc aag gag gaa acc gac tct gta gtg		1308	
Tyr Asp Ile Tyr Glu Lys Gln Thr Lys Glu Glu Thr Asp Ser Val Val			
405	410	415	
ctg ata gaa aac ctg aag aaa gcc tct cag tgatggagat aatttatttt		1358	
Leu Ile Glu Asn Leu Lys Lys Ala Ser Gln			
420	425		
tacccttcaact gtgacccttga gaaga		1383	

<210> 4  
 <211> 426  
 <212> PRT  
 <213> Unknown Organism

<220>  
 <223> Description of Unknown Organism:Human IL-13 receptor  
 alpha-chain

<400> 4

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20 25 30

Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile  
35 40 45

Trp Thr Trp Asn Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu Trp  
50 55 60

Tyr Phe Ser His Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro Glu  
65 70 75 80

Thr Arg Arg Ser Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln  
85 90 95

Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu  
100 105 110

Val Glu Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val  
115 120 125

Thr Glu Leu Gln Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser  
130 135 140

Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr  
145 150 155 160

Tyr Trp His Arg Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile Phe  
165 170 175

Arg Glu Gly Gln Tyr Phe Gly Cys Ser Phe Asp Leu Thr Lys Val Lys  
180 185 190

Asp Ser Ser Phe Glu Gln His Ser Val Gln Ile Met Val Lys Asp Asn  
195 200 205

Ala Gly Lys Ile Lys Pro Ser Phe Asn Ile Val Pro Leu Thr Ser Arg  
210 215 220

Val Lys Pro Asp Pro Pro His Ile Lys Asn Leu Ser Phe His Asn Asp  
225 230 235 240

Asp Leu Tyr Val Gln Trp Glu Asn Pro Gln Asn Phe Ile Ser Arg Cys  
245 250 255

Leu Phe Tyr Glu Val Glu Val Asn Asn Ser Gln Thr Glu Thr His Asn  
260 265 270

Val Phe Tyr Val Gln Glu Ala Lys Cys Glu Asn Pro Glu Phe Glu Arg  
275 280 285

Asn Val Glu Asn Thr Ser Cys Phe Met Val Pro Gly Val Leu Pro Asp  
290 295 300

Thr Leu Asn Thr Val Arg Ile Arg Val Lys Thr Asn Lys Leu Cys Tyr  
305 310 315 320

Glu Asp Asp Lys Leu Trp Ser Asn Trp Ser Gln Glu Met Ser Ile Gly  
325 330 335

Lys Lys Arg Asn Ser Thr Leu Tyr Ile Thr Met Leu Leu Ile Val Pro  
340 345 350

Val Ile Val Ala Gly Ala Ile Ile Val Leu Leu Leu Tyr Leu Lys Arg  
355 360 365

Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe  
370 375 380

Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys  
385 390 395 400

Tyr Asp Ile Tyr Glu Lys Gln Thr Lys Glu Glu Thr Asp Ser Val Val  
405 410 415

Leu Ile Glu Asn Leu Lys Lys Ala Ser Gln  
420 425

<210> 5

<211> 30

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism:signal sequence of murine IL-3

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Leu Leu Met Leu Phe His Leu Gly Leu Gln Ala Ser Ile Ser  
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<210> 6  
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<212> PRT  
<213> Unknown Organism

<220>  
<223> Description of Unknown Organism:N-terminal FLAG epitope-tag

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<210> 7  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Oligo 1478 5'

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31

<210> 8  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Oligo 1480 5'

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aactccacct tctacaccac ctgatctaga

30

<210> 9

<211> 5  
<212> PRT  
<213> Unknown Organism

<220>  
<223> Description of Unknown Organism:NR4 Motif

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<221> Unsure  
<222> (3)  
<223> Xaa may be any amino acid

<400> 9  
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1 5

<210> 10  
<211> 27  
<212> PRT  
<213> Unknown Organism

<220>  
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of mNR4 (major)

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<222> (24)  
<223> Xaa may be any amino acid

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1 5 10 15

Val Gln Pro Pro Val Thr Xaa Leu Ser Val  
20 25

<210> 11  
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mNR4 (minor)

<220>

<221> Unsure

<222> (24)

<223> Xaa may be any amino acid

<400> 11

Ala Ser Ile Ser Ser Asp Tyr Lys Asp Asp Asp Glu Ser Arg Thr Glu  
1 5 10 15

Val Gln Pro Pro Val Thr Xaa Leu Ser Val  
20 25 )